

SEQUENCE LISTING

<110> Berry, Alan
Burlingame, Richard P.
Millis, James R.

<120> PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE

<130> 3161-18-C1

<140>

<141>

<150> PCT/US98/00800

<151> 1998-01-14

<150> 60/035,494

<151> 1997-01-14

<160> 31

<170> PatentIn Ver. 2.0

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 1

cggtctccca tgtgtggaat tggtggcgc

29

<210> 2

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 2

ctctagagcg ttgatattca gtcaattaca aaca

34

<210> 3

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 3
atggatgagc agacgatggt 20

<210> 4
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 4
cctcgaggtc gacggtatc 19

<210> 5
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 5
tggatgagca gacgatgg 18

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 6
tccgtcacag gtatttatcc 20

<210> 7

<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
agctgcgtgg tgcgtac

17

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
ggaccgtggt tcagttcg

18

<210> 9
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
gccgtggcga tcagtac

17

<210> 10
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 10
gccaatcacc agcggac

17

<210> 11

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 11
 atggtttccc gctactgg 18

<210> 12
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 12
 gaaccaaggt aaccagc 18

<210> 13
 <211> 7408
 <212> DNA
 <213> Escherichia coli

<220>
 <221> RBS
 <222> (1240)..(1245)

<220>
 <221> promoter
 <222> (1165)..(1181)

<220>
 <221> conflict
 <222> (2509)..(2510)

<400> 13
 gaattgatcc cgctggttta caacgtcgtg actgggaaaa ccctggcgtt acccaactta 60
 atcgcccttg agcacatccc cctttcgcca gctggcgtaa tagcgaagag gcccgacccg 120
 atcgcccttc ccaacagttg cgcagcctga atggcgaatg gcgctttgcc tggtttccgg 180
 caccagaagc ggtgccggaa agctggctgg agtgcgatct tcctgaggcc gatactgtcg 240

tcgtcccctc aaactggcag atgcacgggt acgatgcgcc catctacacc aacgtaacct 300
atcccattac ggtcaatccg ccgtttgttc ccacggagaa tccgacgggt tgttactcgc 360
tcacatttaa tgttgatgaa agctggctac aggaaggcca gacgcgaatt atttttgatg 420
gcgttaactc ggcgtttcat ctgtggtgca acgggcgctg ggtcggttac ggccaggaca 480
gtcgtttgcc gtctgaattt gacctgagcg cttttttacg cgccggagaa aaccgcctcg 540
cggtgatggg gctgcgttgg agtgacggca gttatctgga agatcaggat atgtggcgga 600
tgagcggcat tttccgtgac gtctcgttgc tgcataaacc gactacacaa atcagcgatt 660
tccatgttgc cactcgcttt aatgatgatt tcagccgcgc tgtactggag gctgaagttc 720
agatgtgcgg cgagttgcgt gactacctac gggtaacagt ttctttatgg cagggtgaaa 780
cgcaggtcgc cagcggcacc gcgcctttcg gcggtgaaat tatcgatgag cgtggtggtt 840
atgccgatcg cgtcacacta cgtctgaacg tcgaaaacc gaaactgtgg agcgccgaaa 900
tcccgaatct ctatcgtcgc gtggttgaac tgcacaccgc cgacggcacg ctgattgaag 960
cagaagcctg cgatgtcggg ttccgcgagg tgcggattga aaatggtctg ctgctgctga 1020
acggcaagcc gttgctgatt cgaggcggtta accgtcacga gcatcatcct ctgcatggtc 1080
aggcatgga tgagcagacg atggtgcagg atctccaccg cggtgggcgc cgctctagaa 1140
ctagtggatc tcgatccgcg gaaattaata cgactcacta taggggaatt gtgagcggat 1200
aacaattccc ctctagaaat aattttgttt aactttaaga aggagatata ccatgtgttg 1260
aattgttggc gcgatcgcgc aacgtgatgt agcagaaatc cttcttgaag gtttacgtcg 1320
tctggaatac cgcggatatg actctgccgg tctggccggt gttgatgcag aaggtcatat 1380
gacccgcctg cgtcgcctcg gtaaagtcca gatgctggca caggcagcgc aagaacatcc 1440
tctgcatggc ggcactggta ttgctcacac tcgctgggcg acccacggtg aaccttcaga 1500
agtgaatgcg catccgcatg tttctgaaca cattgtggtg gtgcataacg gcatcatcga 1560
aaaccatgaa ccgctgcgtg aagagctaaa agcgcgtggc tataccttcg tttctgaaac 1620
cgacaccgaa gtgattgccc atctggtgaa ctgggagctg aaacaaggcg ggactctgcg 1680

tgaggccggtt ctgcgtgcta tcccgcagct gcgtgggtgcg tacggtacag tgatcatgga 1740
 ctcccgtcac ccgataccc tgctggcggc acgttctggt agtccgctgg tgattggcct 1800
 ggggatgggc gaaaacttta tcgcttctga ccagctggcg ctgttgccgg tgacccgtcg 1860
 ctttatcttc cttgaagagg gcgatattgc ggaaatcact cgccgttcgg taaacatctt 1920
 cgataaaact ggcgcggaag taaaacgtca ggatatcgaa tccaatctgc aatatgacgc 1980
 gggcgataaa ggcatttacc gtcactacat gcagaaagag atctacgaac agccgaacgc 2040
 gatcaaaaac acccttaccg gacgcatcag ccacggtcag gttgatttaa gcgagctggg 2100
 accgaacgcc gacgaactgc tgtcgaaggt tgagcatatt cagatcctcg cctgtggtac 2160
 ttcttataac tccggtatgg tttcccgcta ctggtttgaa tcgctagcag gtattccgtg 2220
 cgacgtcgaa atcgccctctg aattccgcta tcgcaaactc gccgtgcgtc gtaacagcct 2280
 gatgatcacc ttgtcacagt ctggcgaaac cgcgataacc ctggctggcc tgcgtctgtc 2340
 gaaagagctg ggttaccttg gttcactggc aatctgtaac gttccgggtt cttctctggt 2400
 gcgcgaatcc gatctggcgc taatgaccaa cgcggttaca gaaatcggcg tggcatccac 2460
 taaagcattc accactcagt taactgtgct gttgatgctg gtggcgaagc tgtctgcct 2520
 gaaaggctctg gatgcctcca ttgaacatga catcgtgcat ggtctgcagg cgctgccgag 2580
 ccgtattgag cagatgctgt ctcaggacaa acgcattgaa gcgctggcag aagatttctc 2640
 tgacaaacat cacgcgctgt tcctggggccg tggcgatcag taccoaatcg cgctggaagg 2700
 cgcattgaag ttgaaagaga tctcttacat tcacgctgaa gcctacgctg ctggcgaact 2760
 gaaacacggt ccgctggcgc taattgatgc cgatatgccg gttattggtt ttgcaccgaa 2820
 caacgaattg ctggaaaaac tgaaatccaa cattgaagaa gttcgcgcgc gtggcgggtca 2880
 gttgtatgtc ttcgccgatc aggatgcggg ttttgtaagt agcgataaca tgcacatcat 2940
 cgagatgccg catgtggaag aggtgattgc accgatcttc tacaccgttc cgctgcagct 3000
 gctggcttac catgtcgcgc tgatcaaagg caccgacgtt gaccagccgc gtaacctggc 3060
 aaaatcggtt acggttgagt aataaatgga tgccctgcgt aagcggggca tttttcttcc 3120

tgttatgttt ttaatcaaac atcctgccaa ctccatgtga caaacctgca tcttcggcta 3180
 ctttttctct gtcacagaat gaaaattttt ctgtcatctc ttcgttatta atgtttgtaa 3240
 ttgactgaat atcaacgctc tagaggggct agagcggccg ccaccgcggt ggagctccgt 3300
 cgacaagctt atcgataccg tcgacctga gggggggccc ggtaccgagg acgcgttcga 3360
 ataaatacct gtgacggaag atcacttcgc agaataaata aatcctgggtg tccctgttga 3420
 taccgggaag ccctgggcca acttttggcg aaaatgagac gttgatcggc acgtaagagg 3480
 ttccaacttt caccataatg aaataagatc actaccgggc gtattttttg agttatcgag 3540
 attttcagga gctaaggaag ctaaaatgga gaaaaaatc actggatata ccaccgttga 3600
 tatatcccaa tggcatcgta aagaacattt tgaggcattt cagtcagttg ctcaatgtac 3660
 ctataaccag accgttcagc tggatattac ggccttttta aagaccgtaa agaaaaataa 3720
 gcacaagttt tatccggcct ttattcacat tcttgcccgc ctgatgaatg ctcatccgaa 3780
 attccgtatg gcaatgaaag acggtgagct ggtgatatgg gatagtgttc acccttggtta 3840
 caccgttttc catgagcaaa ctgaaacggt ttcatcgctc tggagtgaat accacgacga 3900
 tttccggcag tttctacaca tatattcgca agatgtggcg tgttacgggtg aaaacctggc 3960
 ctatttccct aaagggttta ttgagaatat gtttttcgtc tcagccaatc cctgggtgag 4020
 tttcaccagt tttgatttaa acgtggccaa tatggacaac ttcttcgccc ccgttttcac 4080
 catgggcaaa tattatacgc aaggcgacaa ggtgctgatg ccgctggcga ttcagggttca 4140
 tcatgccgtt tgtgatggct tccatgtcgg cagaatgctt aatgaattac aacagtactg 4200
 cgatgagtgg cagggcgggg cgtaattttt ttaaggcagt tattggtgcc cttaaagccc 4260
 tgggtgctacg cctgaataag tgataataag cggatgaatg gcagaaattc ggacgcgtca 4320
 attcgagctc ctgcactgga tgggtggcgt ggatggtaag ccgctggcaa gcggtgaagt 4380
 gcctctggat gtcgctccac aaggtaaaca gttgattgaa ctgcctgaac taccgcagcc 4440
 ggagagcgcc gggcaactct ggctcacagt acgcgtagtg caaccgaacg cgaccgcatg 4500
 gtcagaagcc gggcacatca gcgcctggca gcagtggcgt ctggcggaac acctcagtgt 4560

gacgctcccc gccgctcccc acgccatccc gcatctgacc accagcgaaa tggatttttg 4620
 catcgagctg ggtaataagc gttggcaatt taaccgccag tcaggctttc tttcacagat 4680
 gtggattggc gataaaaaac aactgctgac gccgctgcgc gatcagttca cccgtgcacc 4740
 gctggataac gacattggcg taagtgaagc gacccgcatt gaccctaacg cctgggtcga 4800
 acgctggaag gcggcgggcc attaccaggc cgaagcagcg ttgttgcaat gcacggcaga 4860
 tacacttgct gatgcggtgc tgattacgac cgctcacgcg tggcagcatc aggggaaaac 4920
 cttattttatc agccggaaaa cctaccggat tgatggtagt ggtcaaattg cgattaccgt 4980
 tgatgttgaa gtggcgagcg atacaccgca tccggcgcgg attggcctga actgccagct 5040
 ggcgcaggta gcagagcggg taaactggct cggattaggg ccgcaagaaa actatcccga 5100
 ccgccttact gccgcctgtt ttgaccgctg ggatctgcc a ttgtcagaca tgtatacccc 5160
 gtacgtcttc ccgagcgaaa acggtctgcg ctgcgggacg cgcgaattga attatggccc 5220
 acaccagtgg cgcggcgact tccagttcaa catcagccgc tacagtcaac agcaactgat 5280
 ggaaaccagc catcgccatc tgctgcacgc ggaagaaggc acatggctga atatcgacgg 5340
 tttccatatg cgggtgtgaaa taccgcacag atgcgtaagg agaaaatacc gcatcaggcg 5400
 ctcttccgct tctcgtca ctgactcgct gcgctcggtc gttcggctgc ggcgagcggg 5460
 atcagctcac tcaaaggcgg taatacgggt atccacagaa tcaggggata acgcaggaaa 5520
 gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg cgttgctggc 5580
 gtttttccat aggctccgcc cccctgacga gcatcacaaa aatcgacgct caagtcagag 5640
 gtggcgaaaac ccgacaggac tataaagata ccaggcgttt cccctggaa gctccctcgt 5700
 gcgctctcct gttccgacct tgccgcttac cggataacct tccgcctttc tcccttcggg 5760
 aagcgtggcg ctttctcaat gctcacgctg taggtatctc agttcggtgt aggtcgttcg 5820
 ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg ccttatccgg 5880
 taactatcgt cttgagtcca acccggtgta acacgactta tcgccactgg cagcagccac 5940
 tggtaacagg attagcagag cgaggatatg aggcggtgct acagagttct tgaagtgggtg 6000

gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc tgaagccagt 6060
 taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg ctggtagcgg 6120
 tgggtttttt gtttgcaagc agcagattac ggcagaaaa aaaggatctc aagaagatcc 6180
 tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt aagggatttt 6240
 ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttaaattaaa aatgaagttt 6300
 taaatcaatc taaagtatat atgagtaaac ttggtctgac agttaccaat gcttaatcag 6360
 tgaggcacct atctcagcga tctgtctatt tcgttcaccc atagttgcct gactccccgt 6420
 cgtgtagata actacgatac gggaggggctt accatctggc cccagtgtg caatgatacc 6480
 gcgagacca cgctcaccg ctccagattt atcagcaata aaccagccag ccggaagggc 6540
 cgagcgcaga agtggctctg caactttatc cgcctccatc cagtctatta attgttgccg 6600
 ggaagctaga gtaagtagtt cgccagttaa tagtttgccg aacgttggtt ccattgctac 6660
 aggcacgtg gtgtcacgct cgtcgtttgg tatggcttca ttcagctccg gttcccaacg 6720
 atcaaggcga gttacatgat ccccatgtt gtgcaaaaaa gcggttagct ccttcgggtc 6780
 tccgatcgtt gtcagaagta agttggccgc agtggtatca ctcatggtta tggcagcact 6840
 gcataattct cttactgtca tgccatccgt aagatgcttt tctgtgactg gtgagtactc 6900
 aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt tgctcttgcc cggcgtcaat 6960
 acgggataat accgcgccac atagcagaac tttaaaagtg ctcatcattg gaaaacgttc 7020
 ttcggggcga aaactctcaa ggatcttacc gctgttgaga tccagttcga tgtaaccac 7080
 tcgtgcaccc aactgatctt cagcatcttt tactttcacc agcgtttctg ggtgagcaaa 7140
 aacaggaagg caaaatgccg caaaaaaggg aataaggcg acacggaaat gttgaatact 7200
 catactcttc ctttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg 7260
 atacatattt gaatgtattt agaaaaataa acaaataggg gttccgcgca catttccccg 7320
 aaaagtgcc cctgacgtct aagaaacat tattatcatg acattaacct ataaaaatag 7380
 gcgtatcacg aggccctttc gtcttcaa 7408

<210> 14
 <211> 2184
 <212> DNA
 <213> Escherichia coli

<400> 14
 ccgctctaga actagtggat ctcgatcccg cgaaattaat acgactcact ataggggaat 60
 tgtgagcgga taacaattcc cctctagaaa taattttggt taactttaag aaggagatat 120
 accatgtgtg gaattgttgg cgcgatcgcg caacgtgatg tagcagaaat ctttcttgaa 180
 ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgatgca 240
 gaaggtcata tgaccgcct gcgtcgctc ggtaaagtcc agatgctggc acaggcagcg 300
 gaagaacatc ctctgcatgg cggcactggt attgctcaca ctcgctgggc gaccacggt 360
 gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggt ggtgcataac 420
 ggcatcatcg aaaaccatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480
 gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540
 gggactctgc gtgaggccgt tctgcgtgct atcccgacgc tgcgtggtgc gtacggtaca 600
 gtgatcatgg actcccgta cccggatacc ctgctggcgg cacttcttgg tagtccgctg 660
 gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctgttgccg 720
 gtgaccgctc gctttatctt ccttgaagag ggcgatattg cggaatcac tcgccgttcg 780
 gtaaacaatc tcgataaaac tggcgcggaa gtaaacgctc aggatatcga atccaatctg 840
 caatatgacg cgggcgataa aggcatttac cgtcactaca tgcagaaaga gatctacgaa 900
 cagccgaacg cgatcaaaaa cacccttacc ggacgcatca gccacggtca ggttgattta 960
 agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020
 gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080
 ggtattccgt gcgacgtcga aatcgctct gaattccgct atcgcaaac tgccgtgcgt 1140
 cgtaacagcc tgatgatcac cttgtcacag tctggcgaaa ccgcggatac cctggctggc 1200

ctgcgtctgt cgaaagagct gggttacctt ggttcactgg caatctgtaa cgttccgggt 1260
tcttctctgg tgcgcgaatc cgatctggcg ctaatgacca acgcgggtac agaaatcggc 1320
gtggcatcca ctaaagcatt caccactcag ttaactgtgc tgttgatgct ggtggcgaag 1380
ctgtctcgcc tgaaaggtct ggatgcctcc attgaacatg acatcgtgca tggctctgcag 1440
gcgctgccga gccgtattga gcagatgctg tctcaggaca aacgcattga agcgctggca 1500
gaagatttct ctgacaaaca tcacgcgctg ttcctgggccc gtggcgatca gtaccaatc 1560
gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620
gctggcgaac tgaaacacgg tccgctggcg ctaattgatg ccgatatgcc gggtattggt 1680
gttgaccga acaacgaatt gctggaaaaa ctgaaatcca acattgaaga agttcgcgcg 1740
cgtggcggtc agttgtatgt cttegccgat caggatgcgg gttttgtaag tagcgataac 1800
atgcacatca tcgagatgcc gcatgtggaa gaggtgattg caccgatctt ctacaccgtt 1860
ccgctgcagc tgctggctta ccatgtcgcg ctgatcaaag gcaccgacgt tgaccagccg 1920
cgtaacctgg caaatcgggt tacggttgag taataaatgg atgccctgcg taagcggggc 1980
atctttcttc ctgttatgtt ttaaatcaaa catcctgcc actccatgtg acaaaccgtc 2040
atcttcggct actttttctc tgtcacagaa tgaaaatttt tctgtcatct cttegttatt 2100
aatgtttgta attgactgaa tatcaacgct ctagaggggc tagagcggcc gccaccgcgg 2160
tggagctccg tcgacaagct tatc 2184

<210> 15
<211> 1830
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1830)

<400> 15
atg tgt gga att gtt ggc gcg atc gcg caa cgt gat gta gca gaa atc 48
Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
1 5 10 15

ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc	96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala	
20 25 30	
ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc	144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg	
35 40 45	
ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg	192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu	
50 55 60	
cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa	240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu	
65 70 75 80	
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg	288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val	
85 90 95	
gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta	336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu	
100 105 110	
aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att	384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile	
115 120 125	
gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag	432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu	
130 135 140	
gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg	480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val	
145 150 155 160	
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt	528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly	
165 170 175	
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct	576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser	
180 185 190	
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa	624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu	
195 200 205	

gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat	672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp	
210 215 220	
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa	720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln	
225 230 235 240	
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag	768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu	
245 250 255	
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc	816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile	
260 265 270	
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa	864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu	
275 280 285	
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct	912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser	
290 295 300	
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt	960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly	
305 310 315 320	
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct	1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser	
325 330 335	
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa	1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu	
340 345 350	
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac	1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr	
355 360 365	
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc	1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg	
370 375 380	
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg	1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val	
385 390 395 400	

gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg	1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu	
405 410 415	
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat	1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His	
420 425 430	
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg	1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met	
435 440 445	
ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac	1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp	
450 455 460	
aaa cat cac gcg ctg ttc ctg ggc cgt ggc gat cag tac cca atc gcg	1440
Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala	
465 470 475 480	
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa	1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu	
485 490 495	
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat	1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp	
500 505 510	
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa	1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu	
515 520 525	
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg	1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu	
530 535 540	
tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg	1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met	
545 550 555 560	
cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc	1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe	
565 570 575	
tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa	1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys	
580 585 590	

ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt 1824
 Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
 595 600 605

gag taa 1830
 Glu
 610

<210> 16
 <211> 609
 <212> PRT
 <213> Escherichia coli

<400> 16
 Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
 1 5 10 15

Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
 20 25 30

Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
 130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
 145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
 165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
 180 185 190
 Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
 195 200 205
 Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
 210 215 220
 Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
 225 230 235 240
 Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
 245 250 255
 Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
 260 265 270
 Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
 275 280 285
 Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
 290 295 300
 Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
 305 310 315 320
 Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
 325 330 335
 Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
 340 345 350
 Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
 355 360 365
 Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
 370 375 380
 Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
 385 390 395 400
 Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
 405 410 415
 Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
 420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
 435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
 450 455 460

Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
 465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
 485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
 500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
 515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
 530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
 545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
 565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
 580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
 595 600 605

Glu

<210> 17

<211> 2184

<212> DNA

<213> Escherichia coli

<400> 17

ccgctctaga actagtggat ctcgatcccg cgaaattaat acgactcact ataggggaat 60

tgtgagcgga taacaattcc cctctagaaa taattttggt taactttaag aaggagatat 120

accatgtgtg gaactgttgg cgcgatcgcg caacgtgatg tagcagaaat ccttcttgaa 180

ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgatgca 240
 gaaggtcata tgacccgcct gcgtgcctc ggtaaagtcc agatgctggc acaggcagcg 300
 gaagaacatc ctctgcatgg cggcactggg attgctcaca ctcgctgggc gaccacaggt 360
 gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggg ggtgcataac 420
 ggcatcatcg aaaaccatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480
 gtttctgaaa ccgacaccga agtgattgcc catctgggtga actgggagct gaaacaaggc 540
 gggactctgc gtgaggccgt tctgcgtgct atccgcagc tgcgtggtgc gtacgggtaca 600
 gtgatcatgg actcccgta cccggatacc ctgctggcgg cacgttctgg tagtccgctg 660
 gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctggtgccg 720
 gtgaccgctc gctttatctt ccttgaagag ggcgatattg cggaaatcac tcgccgttcg 780
 gtaaacaatct tcgataaaac tggcgcggaa gtaaaacgtc aggatatcga atccaatctg 840
 caatatgacg cgggcgataa aggcatttac cgtcactaca tgcagaaaga gatctacgaa 900
 cagccgaacg cgatcaaaaa cacccttacc ggacgcacca gccacgggtca ggttgattta 960
 agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020
 gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080
 ggtattccgt gcgacgtcga aatcgctct gaattccgct atcgcaaate tgccgtgcgt 1140
 cgtaacagcc tgatgatcac cttgtcacag tctggcgaaa ccgcggatac cctggctggc 1200
 ctgcgtctgt cgaaagagct gggttacctt ggttcactgg caatctgtaa cgttccgggt 1260
 tcttctctgg tgcgcgaatc cgatctggcg ctaatgacca acgcgggtac agaaatcggc 1320
 gtggcatcca ctaaagcatt caccactcag ttaactgtgc tgttgatgct ggtggcgaag 1380
 ctgtctcgcc tgaaaggctt ggatgcctcc attgaacatg acatcgtgca tggctcgcag 1440
 gcgctgccga gccgtattga gcagatgctg cctcaggaca aacgcattga agcgctggca 1500
 gaagatttct ctgacaaaca tcacgcgctg ttctggggc gtggcgatca gtaccaatc 1560
 gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa	240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu	
65 70 75 80	
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg	288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val	
85 90 95	
gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta	336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu	
100 105 110	
aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att	384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile	
115 120 125	
gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag	432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu	
130 135 140	
gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg	480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val	
145 150 155 160	
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt	528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly	
165 170 175	
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct	576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser	
180 185 190	
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa	624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu	
195 200 205	
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat	672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp	
210 215 220	
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa	720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln	
225 230 235 240	
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag	768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu	
245 250 255	

atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc acc	816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Thr	
260 265 270	
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa	864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu	
275 280 285	
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct	912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser	
290 295 300	
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt	960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly	
305 310 315 320	
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct	1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser	
325 330 335	
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa	1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu	
340 345 350	
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac	1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr	
355 360 365	
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc	1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg	
370 375 380	
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg	1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val	
385 390 395 400	
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg	1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu	
405 410 415	
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat	1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His	
420 425 430	
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg	1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met	
435 440 445	

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Thr
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Pro Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

<210> 20

<211> 2184

<212> DNA

<213> Escherichia coli

<400> 20

ccgctctaga actagtggat ctogatcccg cgaaattaat acgactcact ataggggaat 60

tgtgagcgga taacaattcc cctctagaaa taattttggt taactttaag aaggagatat 120

accatgtgtg gaattgttgg cgcgatcgcg caacgtgatg tagcagaaat ccttcttgaa 180

ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgataca 240

gaaggtcata tgaccgcct gcgtcgccct ggtaaagtcc agatgctggc acaggcagcg 300

gaagaacatc ctctgcatgg cggcactggt attgctcaca ctgctgggc gaccacggt 360

gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggt ggtgcataac 420

ggcatcatcg aaaaccatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480

gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540

gggactctgc gtgaggccgt tctgcgtgct atccccgcagc tgcgtggtgc gtacgggtaca 600
 gtgatcatgg actcccgta cccggatacc ctgctggcgg cacgttcttg tagtccgctg 660
 gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctggtgccg 720
 gtgaccgctc gctttatctt ccttgaagag ggcgatattg cggaatcac tcgccgttcg 780
 gtaaacaatct tcgataaaac tggcgcggaa gtaaaacgtc aggatatcga atccaatctg 840
 caatatgacg cgggcgataa aggcatctac tgtcactaca tgcagaaaga gatctacgaa 900
 cagccgaacg cgatcaaaaa cacccttacc ggacgcatca gccacggtca ggttgattta 960
 agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020
 gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080
 ggtattccgt gcgacgtcga aatcgctcc gaattccgct atcgcaaac tgccgtgcgt 1140
 cgtaacagcc tgatgatcac cttgtcacag tctggcgaac ccgcggatac cctggctggc 1200
 ctgcgtctgt cgaaagagct gggttacctt ggttcaactg caatctgtaa cgttccgggt 1260
 tcttctctgg tgcgcgaatc cgatctggcg ctaatgacca acgcgggtac agaaatcggc 1320
 gtggcatcca ctaaagcatt caccactcag ttaactgtgc tgttgatgct ggtggcgaag 1380
 ctgtctcgcc tgaaaggtct ggatgcctcc attgaacatg acatcgtgca tggctctgag 1440
 gcgctgccga gccgtattga gcagatgctg tctcaggaca aacgcattga agcgctggca 1500
 gaagatttct ctgacaaaca tcacgcgctg ttcctgagcc gtggcgatca gtaccaatc 1560
 gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620
 gctggcgaac tgaaacacgg tccgctggcg ctaattgatg ccgatatgcc ggttattgtt 1680
 gttgcaccga acaacgaatt gctggaaaaa ctgaaatcca acattgaaga agttcgcgcg 1740
 cgtggcggtc agttgtatgt cttcgccgat caggatgcgg gttttgtaag tagcgataac 1800
 atgcacatca tcgagatgcc gcagtggaa gaggtgattg caccgatctt ctacaccgtt 1860
 ccgctgcagc tgctggctta ccatgtcgcg ctgatcaaag gcaccgacgt tgaccagccg 1920
 cgtaacctgg caaaatcggg tacggttgag taataaatgg atgcctgcg taagcggggc 1980

- attttttcttc ctgttatgtt tttaatcaaa catcctgcc aactccatgtg acaaaccgtc 2040
 atcttcgggt actttttctc tgtcacagaa tgaaaatttt tctgtcatct ctctcgttatt 2100
 aatgtttgta attgactgaa tatcaacgct ctaggggggc tagagcggcc gccaccgcgg 2160
 tggagctccg tcgacaagct tacc 2184

<210> 21
 <211> 1830
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1830)

<400> 21
 atg tgt gga att gtt ggc gcg atc gcg caa cgt gat gta gca gaa atc 48
 Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
 1 5 10 15
 ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
 Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
 20 25 30
 ggt ctg gcc gtt gtt gat aca gaa ggt cat atg acc cgc ctg cgt cgc 144
 Gly Leu Ala Val Val Asp Thr Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45
 ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
 Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60
 cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240
 His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80
 cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg 288
 Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95
 gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta 336
 Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110
 aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att 384

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag 432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg 480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt 528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct 576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa 624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat 672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa 720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

tat gac gcg ggc gat aaa ggc att tac tgt cac tac atg cag aaa gag 768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu
245 250 255

atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc 816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa 864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct 912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt 960

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

att ccg tgc gac gtc gaa atc gcc tcc gaa ttc cgc tat cgc aaa tct 1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa 1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

acc gcg gat acc ctg gct ggc ctg cgt ctg tcc aaa gag ctg ggt tac 1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc 1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg 1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg 1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat 1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg 1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac 1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg 1440
Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa 1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat 1536

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa 1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg 1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg 1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc 1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa 1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt 1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

gag taa 1830
Glu
610

<210> 22

<211> 609

<212> PRT

<213> Escherichia coli

<400> 22

Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
1 5 10 15

Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

Gly Leu Ala Val Val Asp Thr Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu

50	55	60
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu		
65	70	75 80
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val		
	85	90 95
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu		
	100	105 110
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile		
	115	120 125
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu		
	130	135 140
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val		
	145	150 155 160
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly		
	165	170 175
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser		
	180	185 190
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu		
	195	200 205
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp		
	210	215 220
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln		
	225	230 235 240
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu		
	245	250 255
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile		
	260	265 270
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu		
	275	280 285
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser		
	290	295 300
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly		

305					310					315					320
Ile	Pro	Cys	Asp	Val	Glu	Ile	Ala	Ser	Glu	Phe	Arg	Tyr	Arg	Lys	Ser
				325					330					335	
Ala	Val	Arg	Arg	Asn	Ser	Leu	Met	Ile	Thr	Leu	Ser	Gln	Ser	Gly	Glu
			340					345					350		
Thr	Ala	Asp	Thr	Leu	Ala	Gly	Leu	Arg	Leu	Ser	Lys	Glu	Leu	Gly	Tyr
		355					360					365			
Leu	Gly	Ser	Leu	Ala	Ile	Cys	Asn	Val	Pro	Gly	Ser	Ser	Leu	Val	Arg
	370					375					380				
Glu	Ser	Asp	Leu	Ala	Leu	Met	Thr	Asn	Ala	Gly	Thr	Glu	Ile	Gly	Val
385					390					395					400
Ala	Ser	Thr	Lys	Ala	Phe	Thr	Thr	Gln	Leu	Thr	Val	Leu	Leu	Met	Leu
				405					410					415	
Val	Ala	Lys	Leu	Ser	Arg	Leu	Lys	Gly	Leu	Asp	Ala	Ser	Ile	Glu	His
			420					425					430		
Asp	Ile	Val	His	Gly	Leu	Gln	Ala	Leu	Pro	Ser	Arg	Ile	Glu	Gln	Met
		435					440					445			
Leu	Ser	Gln	Asp	Lys	Arg	Ile	Glu	Ala	Leu	Ala	Glu	Asp	Phe	Ser	Asp
	450					455					460				
Lys	His	His	Ala	Leu	Phe	Leu	Ser	Arg	Gly	Asp	Gln	Tyr	Pro	Ile	Ala
465					470					475					480
Leu	Glu	Gly	Ala	Leu	Lys	Leu	Lys	Glu	Ile	Ser	Tyr	Ile	His	Ala	Glu
				485					490					495	
Ala	Tyr	Ala	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Ile	Asp
			500					505					510		
Ala	Asp	Met	Pro	Val	Ile	Val	Val	Ala	Pro	Asn	Asn	Glu	Leu	Leu	Glu
		515					520					525			
Lys	Leu	Lys	Ser	Asn	Ile	Glu	Glu	Val	Arg	Ala	Arg	Gly	Gly	Gln	Leu
	530					535					540				
Tyr	Val	Phe	Ala	Asp	Gln	Asp	Ala	Gly	Phe	Val	Ser	Ser	Asp	Asn	Met
545					550					555					560
His	Ile	Ile	Glu	Met	Pro	His	Val	Glu	Glu	Val	Ile	Ala	Pro	Ile	Phe

565

570

575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
 580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
 595 600 605

Glu

<210> 23

<211> 2184

<212> DNA

<213> Escherichia coli

<400> 23

ccgctctaga actagtggat ctcgatcccg cgaaattaat acgactcact ataggggaat 60
 tgtgagcggg taacaattcc cctctagaaa taattttgtt taactttaag aaggagatat 120
 accatgtgtg gaattgttgg cgcgatcgcg caacgtgatg tagcagaaat ccttcttgaa 180
 ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgatgca 240
 gaaggtcata tgacccgcct gcgtgcctc ggtaaagtcc agatgctggc acaggcagcg 300
 gaagaacatc ctctgcatgg cggcactggg attgctcaca ctgctgggc gaccacggg 360
 gaaccttcag aagtgaatgc gcatccgcat gtttccgaac acattgtggg ggtgcataac 420
 ggcacatcgc aaaacatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480
 gtttctgaaa ccgacaccga agtgattgcc catctgggtga actgggagct gaaacaaggc 540
 gggactctgc gtgaggccgt tctgcgtgct atcccgcagc tgcgtggtgc gtacggtaca 600
 gtgatcatgg actcccgta cccggatacc ctgctggcgg cacgttctgg tagtccgctg 660
 gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctggtgccg 720
 gtgacccgtc gctttatctt ccttgaagag ggcgatattg cggaaatcac tcgccgttcg 780
 gtaaacaatc tcgataaaac tggcgcggaa gtaaaacgtc aggatatcga atccaatctg 840
 caatatgacg cgggcgataa aggcatttac cgtcactaca tgcagaaaga gatctacgaa 900
 cagccgaacg cgatcaaaaa cacccttacc ggacgcatca gccacggtca ggttgattta 960

agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020
gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080
ggatttccgt gcgacgtcga aatcgctctt gaattccgct atcgcaaata tgcctgtcgt 1140
cgtaacagcc tgatgatcac cttgtcacag tctggcgaaa ccgcggtata cctggctggc 1200
ctgcgtctgt cgaaagagct gggttacctt ggttcaactg caatctgtaa cgttccgggt 1260
tcttctctgg tgcgcgaata cgatctggcg ctaatgacca acgcggttac agaaatcggc 1320
gtggcatcca ctaaagcatt caccactcag ttaactgtgc tgttgatgct ggtggcgaag 1380
ctgtctcgcc tgaaaggtct ggatgcctcc attgaacatg acatcgtgca tggctctgag 1440
gcgctgccga gccgtattga gcagatgctg tctcaggaca aacgcattga agcgctggca 1500
gaagatttct ctgacaaaca tcacgcgccg ttcctgggccc gtggcgatca gtaccaatac 1560
gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620
gctggcgaaac tgaaacacgg tccgctggcg ctaattgatg ccgatatgcc ggttattgtt 1680
gttgaccga acaacgaatt gctggaaaaa ctgaaatcca acattgaaga agttcgcgcg 1740
cgtggcggtc agttgtatgt cttcgccgat caggatgcgg gttttgtaag tagcgataac 1800
atgcacatca tcgagatgcc gcatgtggaa gaggtgattg caccgatctt ctacaccgtt 1860
ccgctgcagc tgctggctta ccatgtcgcg ctgatcaaag gcaccgacgt tgaccagccg 1920
cgtaacctgg caaaatcggg tacggttgag taataaatgg atgccctgcg taagcggggc 1980
atcttcttct ctgttatgtt tttaatcaaa catcctgcc actccatgtg acaaaccgtc 2040
atcttcggct actttttctc tgtcacagaa tgaaaatttt tctgtcatct cttcgttatt 2100
aatgtttgta attgactgaa tatcaacgct ctagaggggc tagagcggcc accaccgcgg 2160
tggagctccg tcgacaagct tatc 2184

<210> 24
<211> 1830
<212> DNA
<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1830)

<400> 24

atg tgt gga att gtt ggc gcg atc gcg caa cgt gat gta gca gaa atc 48
Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
1 5 10 15

ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

cct tca gaa gtg aat gcg cat ccg cat gtt tcc gaa cac att gtg gtg 288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta 336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att 384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag 432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg 480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt 528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly

165	170	175	
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct			576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser			
180	185	190	
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa			624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu			
195	200	205	
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat			672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp			
210	215	220	
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa			720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln			
225	230	235	240
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag			768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu			
245	250	255	
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc			816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile			
260	265	270	
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa			864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu			
275	280	285	
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct			912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser			
290	295	300	
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt			960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly			
305	310	315	320
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct			1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser			
325	330	335	
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa			1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu			
340	345	350	
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac			1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr			

355	360	365	
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc			1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg			
370	375	380	
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg			1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val			
385	390	395	400
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg			1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu			
405	410	415	
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat			1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His			
420	425	430	
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg			1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met			
435	440	445	
ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac			1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp			
450	455	460	
aaa cat cac gcg ccg ttc ctg ggc cgt ggc gat cag tac cca atc gcg			1440
Lys His His Ala Pro Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala			
465	470	475	480
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa			1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu			
485	490	495	
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat			1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp			
500	505	510	
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa			1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu			
515	520	525	
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg			1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu			
530	535	540	
tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg			1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met			

545	550	555	560	
cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc				1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe				
	565	570	575	
tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa				1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys				
	580	585	590	
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt				1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val				
	595	600	605	
gag taa				1830
Glu				
	610			
<210> 25				
<211> 609				
<212> PRT				
<213> Escherichia coli				
<400> 25				
Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile				
1 5 10 15				
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala				
20 25 30				
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg				
35 40 45				
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu				
50 55 60				
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu				
65 70 75 80				
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val				
85 90 95				
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu				
100 105 110				
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile				
115 120 125				

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Pro Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

<210> 26

<211> 2184

<212> DNA

<213> Escherichia coli

<400> 26

ccgctctaga actagtggat ctcgatcccg cgaaattaat acgactcact ataggggaat 60
tgtgagcggg taacaattcc cctctagaaa taattttgtt taactttaag aaggagatat 120
accatgtgtg gaattgttgg cgcgatcgcg caacgtgatg tagcagaaat ctttcttgaa 180
ggtttacgtc gtctggaata ccgcggatat gactctgccg gtctggccgt tgttgatgca 240
gaaggtcata tgacccgcct gcgtcgccct ggtaaagtcc agatgctggc acaggcagcg 300
gaagaacatc ctctgcatgg cggcactggg attgctcaca ctcgctgggc gaccacgggt 360
gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggg ggtgcataac 420
ggcatcatcg aaaaccatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480
gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540
gggactctgc gtgaggccgt tctgcgtgct atccgcagc tgcgtggtgc gtacggtaca 600
gtgatcatgg actcccgta cccggatacc ctgctggcgg caggttctgg tagtccgctg 660
gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctgttgccg 720
gtgaccgctc gctttatctt ccttgaagag ggcgatattg cggaatcac tcgccgttcg 780
gtaaacatct tcgataaaac tggcgcggaa gtaaaacgtc aggatatcga atccaatctg 840
caatatgacg cgggcgataa aggcatttac cgtcactaca tgcagaaaga gatctacgaa 900
cagccgaacg cgatcaaaaa cacccttacc ggacgcacga gccacggtca ggttgattta 960
agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020
gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080
ggattccgt gcgacgtcga aatcgccctt gaattccgct atcgcaaac tgccgtgcgt 1140
cgtaacagcc tgatgatcac cttgtcacag tctggcgaaa ccgcggatac cctggctggc 1200
ctgcgtctgt cgaaagagct gggttacctt ggttcactgg caatctgtaa cgttccgggt 1260
tcttctctgg tgcgcgaatc cgatctggcg ctaatgacca acgcgggtac agaaatcggc 1320

gtggcatcca ctaaagcatt caccactcag ttaactgtgc tgttgatgct ggtggcgaag 1380
 ctgtctcgcc tgaaaggtct ggatgcctcc attgaacatg acatcgtgca tggctctgcag 1440
 gcgctgccga gccgtattga gcagatgctg tctcaggaca aacgcattga agcgctggca 1500
 gaagatttct ctgacaaaca tcacgcgctg ttcctgagcc gtggcgatca gtaccaatc 1560
 gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620
 gctggcgaac tgaaacacgg tccgctggcg ctaattgatg ccgatatgcc gggtattgtt 1680
 gttgcaccga acaacgaatt gctggaaaaa ctgaaatcca acattgaaga agttcgcgcg 1740
 cgtggcggtc agttgtatgt cttcgccgat caggatgcgg gttttgtaag tagcgataac 1800
 atgcacatca tcgagatgcc gcattgtgaa gaggtgattg caccgatctt ctacaccgtt 1860
 ccgctgcagc tgctggctta ccatgtcgcg ctgatcaaag gcaccgacgt tgaccagccg 1920
 cgtaacctgg caaaatcggt tacggttgag taataaatgg atgccctgcg taagcggggc 1980
 atttttcttc ctgttatgtt tttaatcaaa catcctgcc aactccatgtg acaaaccgtc 2040
 atcttcgggt actttttctc tgtcacagaa tgaaaatttt tctgtcatct cttcgttatt 2100
 aatgtttgta attgactgaa tatcaacgct ctaggggggc tagagcggcc gccaccgcgg 2160
 tggagctccg tcgacaagct tatc 2184

<210> 27
 <211> 1830
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1830)

<400> 27
 atg tgt gga att gtt ggc gcg atc gcg caa cgt gat gta gca gaa atc 48
 Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
 1 5 10 15
 ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
 Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
 20 25 30

ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc	144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg	
35 40 45	
ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg	192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu	
50 55 60	
cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa	240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu	
65 70 75 80	
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg	288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val	
85 90 95	
gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta	336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu	
100 105 110	
aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att	384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile	
115 120 125	
gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag	432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu	
130 135 140	
gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg	480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val	
145 150 155 160	
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt	528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly	
165 170 175	
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct	576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser	
180 185 190	
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa	624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu	
195 200 205	
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat	672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp	
210 215 220	

aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa	720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln	
225 230 235 240	
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag	768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu	
245 250 255	
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga_cgc atc	816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile	
260 265 270	
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa	864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu	
275 280 285	
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct	912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser	
290 295 300	
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt	960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly	
305 310 315 320	
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct	1008
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser	
325 330 335	
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa	1056
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu	
340 345 350	
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac	1104
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr	
355 360 365	
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc	1152
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg	
370 375 380	
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg	1200
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val	
385 390 395 400	
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg	1248
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu	
405 410 415	

gag taa
Glu
610

1830

<210> 28
<211> 609
<212> PRT
<213> Escherichia coli

<400> 28
Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
1 5 10 15
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

gaagaacatc ctctgcatgg cggcactggt attgctcaca ctgctgggc gaccacggt 360
 gaaccttcag aagtgaatgc gcatccgcat gtttctgaac acattgtggt ggtgcataac 420
 ggcatcatcg aaaacatga accgctgcgt gaagagctaa aagcgcgtgg ctataccttc 480
 gtttctgaaa ccgacaccga agtgattgcc catctggtga actgggagct gaaacaaggc 540
 gggactctgc gtgaggccgt tctgcgtgct atccgcagc tgcgtggtgc gtacggtaca 600
 gtgatcatgg actcccgta cccggatacc ctgctggcgg cacgttctgg tagtccgctg 660
 gtgattggcc tggggatggg cgaaaacttt atcgcttctg accagctggc gctgttgccg 720
 gtgaccgctc gctttatctt ccttgaagag ggcgatattg cggaaatcac tcgccgttcg 780
 gtaaacaatc tcgataaaac tggcgcggaa gtaaaacgctc aggatatcga atccaatctg 840
 caatatgacg cgggcgataa aggcatttac cgtcactaca tgcagaaaga gatctacgaa 900
 cagccgaacg cgatcaaaaa cacccttacc ggacgcatca gccacggtca ggttgattta 960
 agcgagctgg gaccgaacgc cgacgaactg ctgtcgaagg ttgagcatat tcagatcctc 1020
 gcctgtggta cttcttataa ctccggtatg gtttcccgct actggtttga atcgctagca 1080
 ggtattccgt gcgacgtcga aatcgctct gaattccgct atcgcaaate tgcgctgcgt 1140
 cgtaacagcc tgatgatcac cttgtcacag tctggcgaaa ccgcggatac cctggctggc 1200
 ctgctctgt cgaaagagct gggttacctt gggttactgg caatctgtaa cgttccgggt 1260
 tcttctctgg tgcgcgaatc cgatctggcg ctaatgacca acgcgggtac agaaatcggc 1320
 gtggcatcca ctaaagcatt caccactcag ttaactgtgc tggtgatgct ggtggcgaag 1380
 ctgtctcgcc tgaaaggctt ggatgcctcc attgaacatg acatcgtgca tggctctgcag 1440
 gcgctgccga gccgtattga gcagatgctg tctcaggaca aacgcattga agcgtggca 1500
 gaagatttct ctgacaaaca tcacgcgtg ttcctgagcc gtggcgatca gtaccaatc 1560
 gcgctggaag gcgcattgaa gttgaaagag atctcttaca ttcacgctga agcctacgct 1620
 gctggcgaac tgaaacacgg tccgctggcg ctaattgatg ccgatatgcc ggttattgtt 1680
 gttgcaccga acaacgaatt gctggaaaaa ctgaaatcca acattgaaga agttcgcgcg 1740

cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg	288
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val	
85 90 95	
gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta	336
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu	
100 105 110	
aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att	384
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile	
115 120 125	
gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag	432
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu	
130 135 140	
gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg	480
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val	
145 150 155 160	
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt	528
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly	
165 170 175	
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct	576
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser	
180 185 190	
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa	624
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu	
195 200 205	
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat	672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp	
210 215 220	
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa	720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln	
225 230 235 240	
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag	768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu	
245 250 255	
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc	816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile	
260 265 270	

agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa 864
 Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
 275 280 285

ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct 912
 Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
 290 295 300

tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt 960
 Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
 305 310 315 320

att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct 1008
 Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
 325 330 335

gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa 1056
 Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
 340 345 350

acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac 1104
 Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
 355 360 365

ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc 1152
 Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
 370 375 380

gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg 1200
 Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
 385 390 395 400

gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg 1248
 Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
 405 410 415

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat 1296
 Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
 420 425 430

gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg 1344
 Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
 435 440 445

ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac 1392
 Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
 450 455 460

1	5	10	15
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala			
20	25	30	
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg			
35	40	45	
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu			
50	55	60	
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu			
65	70	75	80
Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val			
85	90	95	
Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu			
100	105	110	
Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile			
115	120	125	
Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu			
130	135	140	
Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val			
145	150	155	160
Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly			
165	170	175	
Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser			
180	185	190	
Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu			
195	200	205	
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp			
210	215	220	
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln			
225	230	235	240
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu			
245	250	255	
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile			

260	265	270
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu		
275	280	285
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser		
290	295	300
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly		
305	310	315 320
Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser		
325	330	335
Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu		
340	345	350
Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr		
355	360	365
Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg		
370	375	380
Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val		
385	390	395 400
Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu		
405	410	415
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His		
420	425	430
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met		
435	440	445
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp		
450	455	460
Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala		
465	470	475 480
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu		
485	490	495
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp		
500	505	510
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu		

515

520

525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
 530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
 545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
 565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
 580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
 595 600 605

Glu